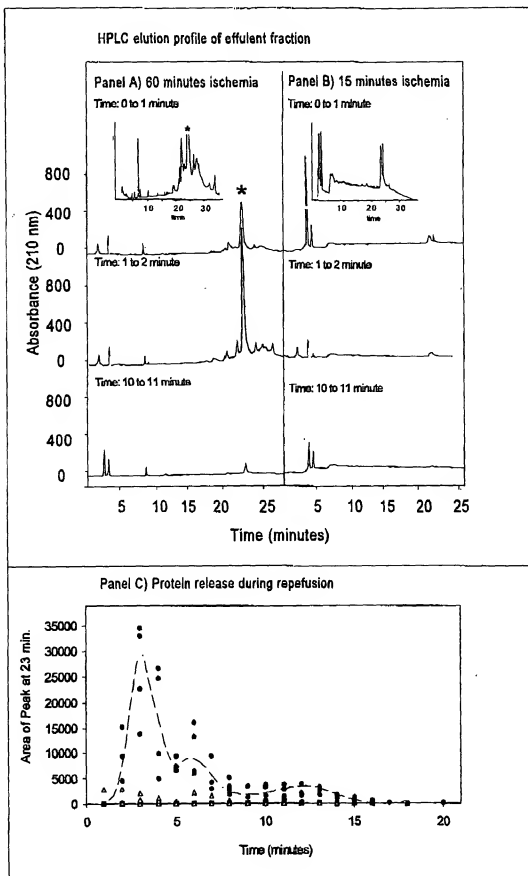


FIGURE 1

FIGURE 2



985T40-025T160

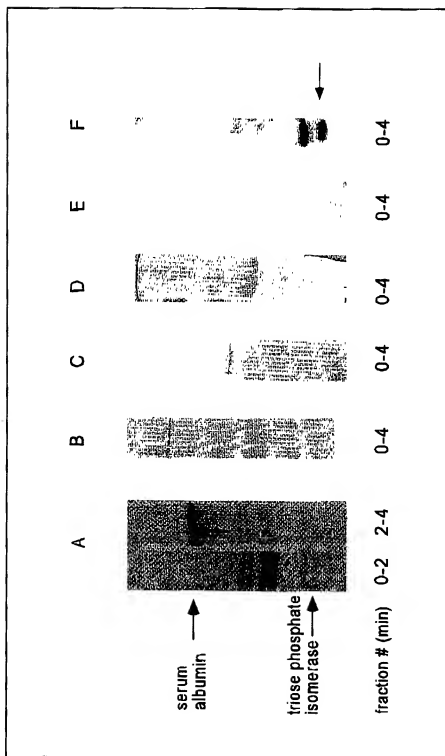


FIGURE 3

**FIGURE 4**

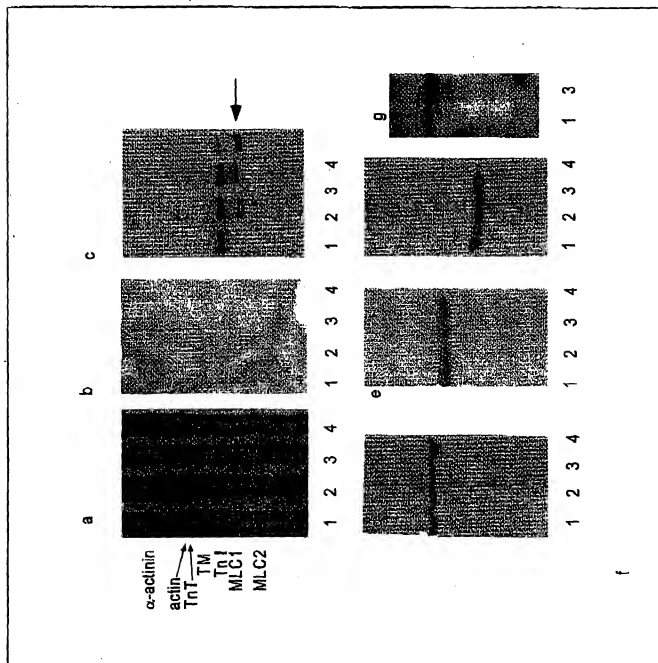
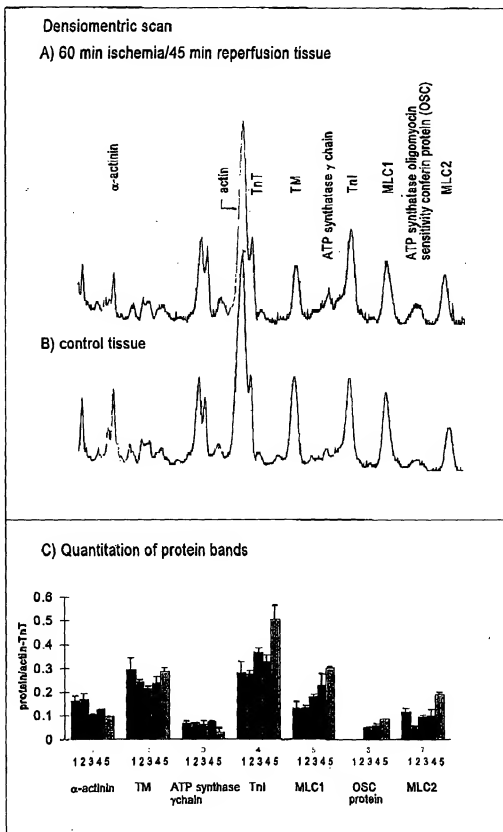


FIGURE 5



0015589-071598

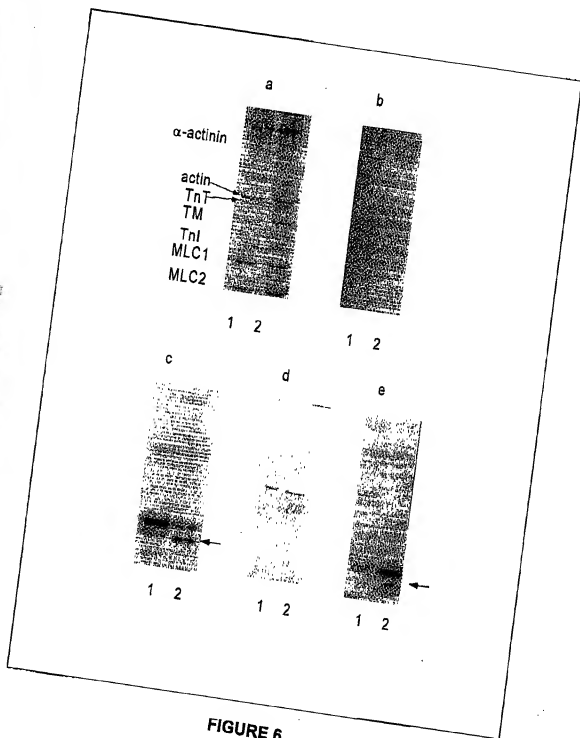


FIGURE 6

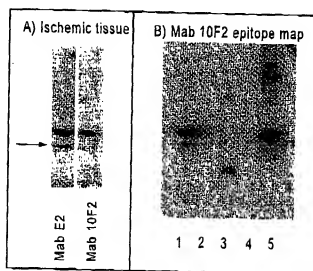
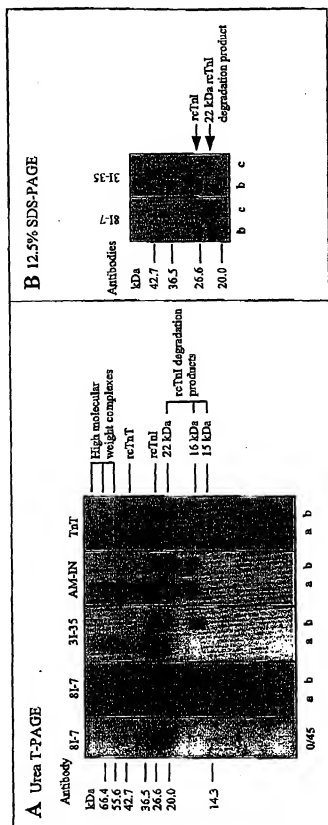


FIGURE 7

00115560 071400 0051400

FIGURE 8





Q. 2. How many of the following are correct?

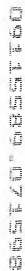
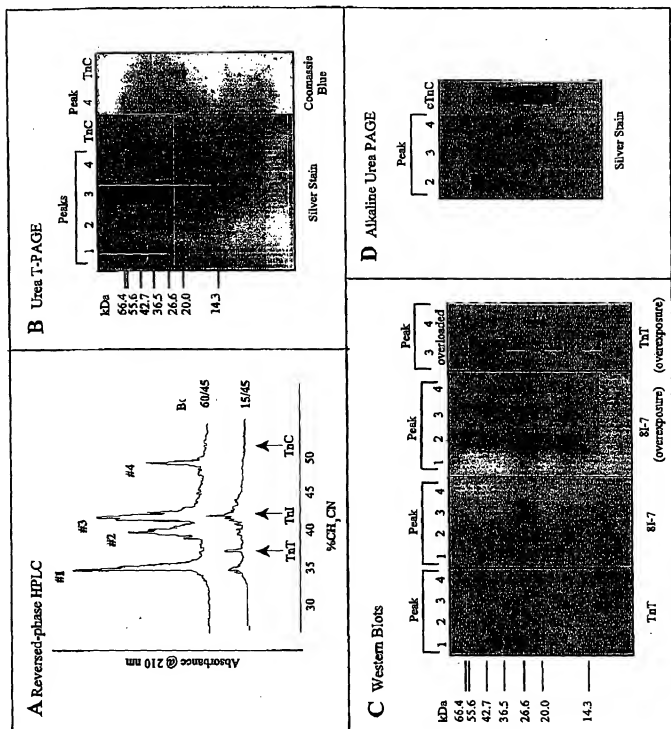


FIGURE 10



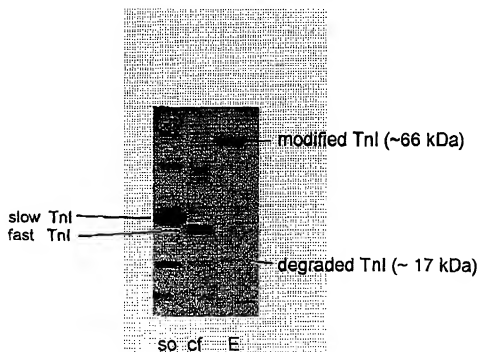


FIGURE 11

00415589.071598

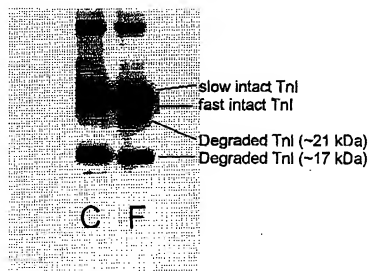


FIGURE 12A

00115800-071598

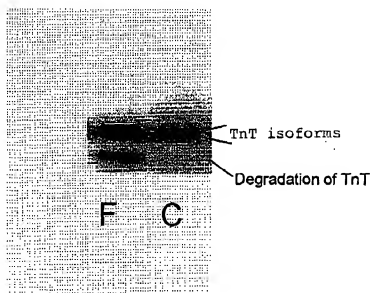
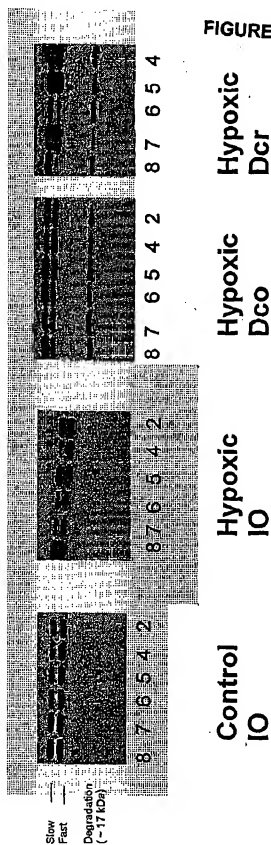


FIGURE 12B

00115589.071598

B65T20'6855T10



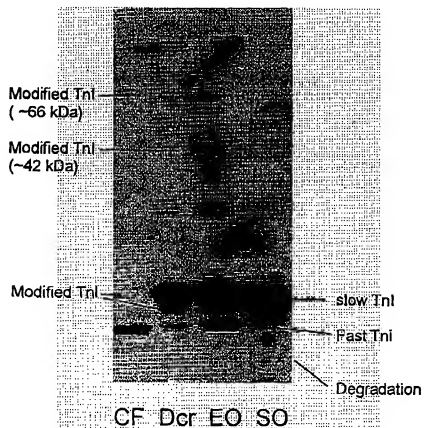


FIGURE 13B

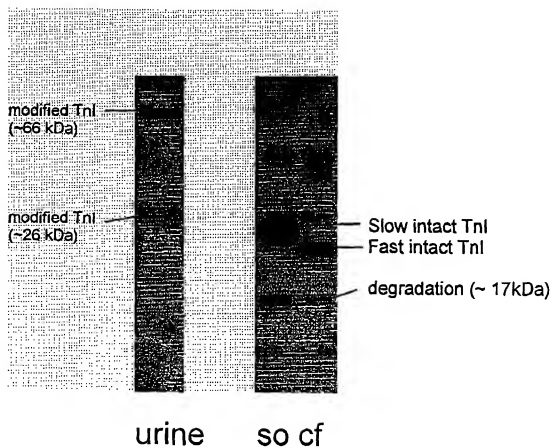


FIGURE 14

00115330.071508



FIGURE 15

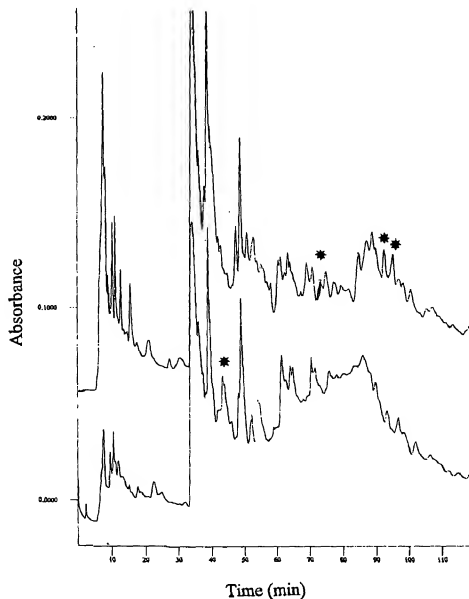
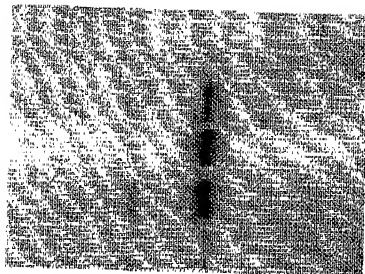


Figure . HPLC analysis of normoxic (bottom trace ) and hypoxic urine (top trace) displayed at 278 nm. Some differences are noted with an asterisk. Each peak represents one or more proteins. The proteins were eluted with a 20 min isocratic wash (100 %A) followed by a linear gradient to 110 min (72% A; 28 % B) followed by another linear gradient to 120 min (20 % A; 80 %B). A-0.05% TFA in HOH; B-0.05% TFA in Acetonitrile.

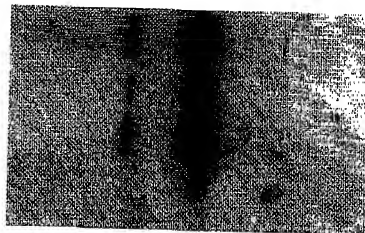
FIGURE 16

Patient #2



L V LV RU RU  
before after before after

Patient #1



L Vague RU RU  
before after before after  
Water

complex ↑

intact troponin I ↑

degradation products  
of troponin I →

→

*Human Troponin I*

cardiac	ADGSSDAARE	PRPAPAPIRR	RSSNYRAYAT	EPHAKKSKI	SASRKLQKLT
slow skeletal	.....	.....	.....	PEVERKPKI	TASRKLKLS
fast skeletal	.....	.....	.....	GDEEKNRA	ITARRQHLKS
cardiac	LLLQIAKQEL	EREAERRGE	KGRALSTRQ	PLELAGLGA	ELQDLCRQLH
slow skeletal	LMLAKAKECW	EQEHEERAE	KVRYLAERIP	TLQTRGLSL	ALQDLCRELH
fast skeletal	VMLQIAATEL	EKEESRRRAE	KONYLAERCP	PLHIPG.SMS	EVOELCKQLH
cardiac	ARVDKVDEER	YDIEAKVTKN	ITEIADLTQK	IFDLRGKPKR	PTLRRVRISA
slow skeletal	AKVEVVDEER	YDIEAKCLHN	TREIKDLKLK	VMDLRGKPKR	PPLRRVRVSA
fast skeletal	AKIDAAEESK	YDMEVRVQKT	SKELEDMNQK	LFDLRGKPKR	PPLRRVRMSA
cardiac	DAMMOALLGA	RAKESLDLRA	HLKQVKKEDT	EKEN...REV	GDWRKNIDAL
slow skeletal	DAMLRALLGS	KHKVSMDLRA	NLKS VKKEDT	EKER...PVEV	GDWRKNVEAM
fast skeletal	DAMLKALLGS	KHKVCMDLRA	NLKQVKKEDT	EKERDL.RDV	GDWRKNIEEK
cardiac	SGMEGRKKKF	ES.....			
slow skeletal	SGMEGRKKMF	DAKSPTSQ			
fast skeletal	SGMEGRKKMF	ES.....			

1. Cardiac.....209 amino acids.....(P19429 - swiss prot identification number)  
VALLINS W.J., *et. al.*  
*FEBS LETT.* 270:57-61, 1990.
2. slow.....186 amino acids.....(P19237 - swiss prot identification number)  
WADE R., *et. al.*  
*GENOMICS* 7:346-357, 1990.
3. fast.....181 amino acids.....(P48788 - swiss prot identification number)  
ZHU L., *et. al.*  
*BIOCHIM. BIOPHYS. ACTA* 1217:338-340, 1994.

Sequences (1:2) Aligned. Score: 60  
 Sequences (1:3) Aligned. Score: 54  
 Sequences (2:3) Aligned. Score: 56

FIGURE 17A

## Rat Troponin I

Human Cardiac	ADGSSDAARE	PRPAPAPIRR	RS.SNYRAYA	TEPHAKKKSK	TSASRKLQLK
Rat Cardiac	ADESSDAAGE	PQPAPAPFVR	ASSANTRAYA	TEPHAKKKSK	TSASRKLQLK
Rat Slow	.....	.....	.....	..FEVERKSK	ITASRKLMLK
Rat Fast	.....	.....	.....	..GDEKRNRR	AITARRQHLLK
Human Cardiac	TLLLQIAKQE	LEREAERERG	EKGRALSTRC	QPLELAGLGF	AELQDLCRQL
Rat Cardiac	TLMLQIAKQE	MEREAERERG	EKGRVLSTRC	QPLVLDLQGP	BELODLCRQL
Rat Slow	SLMLAKAKEC	WEQHEEREA	EKVRYLSERI	PTLQTRGLSL	SALQDLCREL
Rat Fast	SVMLQIAATE	LEKEESRRER	EKQNYLSEHC	PPLWIFGFS	SEVQELCRQL
Human Cardiac	HARVDKVDEE	RYDIEAKVTK	NITEIADLTQ	KIPDLRGKFK	RPTLRVRVRS
Rat Cardiac	HARVDKVDEE	RYDVSAKVTK	NITEIADLTQ	KIYDLRGKFK	RPTLRVRVRS
Rat Slow	HAKVEVVDDEE	RYDIEAKCLH	NTRKIDKLKL	KVLDLRGKFK	RPPLRRVRVS
Rat Fast	HAKIDAAEES	KYDMEVKVOK	SKKELEDMMQ	KLPDLRGKFK	RPPLRRVRVS
Human Cardiac	ADAMMQALLG	ARAKESLDLR	AHLKQVKKED	TEKEN...RE	VGDWRKNIDA
Rat Cardiac	ADAMMQALLG	TRAKESLDLR	AHLKQVKKED	IEKEN...RE	VGDWRKNIDA
Rat Slow	ADAMLRALLG	SKHKVSMDLR	ANLKSQVKKED	TEKER...PVE	VGDWRKNVEA
Rat Fast	ADAMLRALLG	SKHKVCMDLR	ANLKSQVKKED	TEKERDL.RD	VGDWRKNIEE
Human Cardiac	LSGMEGRKKK	FES.....	.....	.....	.....
Rat Cardiac	LSGMEGRKKK	FEG.....	.....	.....	.....
Rat Slow	MSGMEGRKKM	FDAAKSPTLQ	.....	.....	.....
Rat Fast	MSGMEGRKKM	FESES.....	.....	.....	.....

- Human cardiac TnI...209 amino acids (P19429 - swiss prot identification number)  
VALLINS W.J., *et al.*  
*FEBS LETT.* 270:57-61,1990.
- Rat Cardiac TnI.....210 amino acids (P23693 - swiss prot identification number)  
MURPHY A.M., *et al.*  
*BIOCHEMISTRY* 30:707-712, 1991.
- Rat slow TnI.....186 amino acids (P13413 - swiss prot identification number)  
KOPPE R.I., *et al.*  
*J. BIOL. CHEM.* 264:14327-14333, 1989.
- Rat fast TnI.....181 amino acids (P27768 - swiss prot identification number)  
GRAVEL M., HASTINGS K.E.;  
SUBMITTED (XXX-1991) TO EMBL/GENBANK/DBJ DATA BANKS.

Sequences (1:2) Aligned. Score: 92  
 Sequences (1:3) Aligned. Score: 61  
 Sequences (1:4) Aligned. Score: 55  
 Sequences (2:3) Aligned. Score: 60  
 Sequences (2:4) Aligned. Score: 54  
 Sequences (3:4) Aligned. Score: 56

FIGURE 17B

## Human Troponin T

Cardiac	SDIEFVEEY EEEQEEAAV EEQEAAESD ARAAEETET RAEDEEEES
Slow skeletal	SDTEE..QEY EEEQEEAAA EE.....EEE APPE..PEP. VAE.....
fast skeletal	SD.EE.VEQV EEQYEEEEE QE.....EEE VQED..TAE DA.....
Cardiac	AKAEADGPM ESKPKP.RSP MPNLVPPKIP DGERVDFDDI HRKRMKDLN
Slow skeletal	.....PEE E.RPKPSRPV VPPLIPKIP EGERVDFDDI HRKRMKDLL
fast skeletal	.....EE K..FRP.....KLTAIPKIP EGEKVDFFDI QKKRQNKDLM
Cardiac	ELQALISAHF ENRKEEEEL VSLKDRIER RAERAEQQRI RNRKEKERQN
Slow skeletal	ELQTLIDVHF EQRKKEEEL VALKERIER RSEKAEQQRF RTEKERERQA
fast skeletal	ELQALIDSHF EARKKEEEL VALKERIEK RAERAEQQRI RAEKERERQN
Cardiac	RLAEERARRE EENRRKRAED EARKKKALSN M.MHFGGYIQ KQAQTERKSG
Slow skeletal	KLAEERMRKE EEEAKKRAED DAKKKKVLN MGAHFGGYLV KAEQK.R..G
fast skeletal	RLAEERARRE EDAKKRAED DLKKKKALSS MGANYSSYLA KADQK.R..G
Cardiac	KROTERRKKK KILAERRKVL AIDHLMEDQL R.....EKA
Slow skeletal	KROTGREMKV RILSERKKPL DIDMGEEQL KARSALPPS OPSCPAREKA
fast skeletal	KKQTAREMKK KILAERRKPL NIDHLGEDKL R.....DKA
Cardiac	KELWQSIYNL EAEKFDLQEK FKQOKVEINV LRNRINDNQK VSKTRG...K
Slow skeletal	QELSDWIHQL ESEKFDLMAK LKQOKVEINV LYNRISHAQK FRKAG...K
fast skeletal	KELWETLHQL EIDKFEPGEK LKRQKYDITT LRSRIDQAQK HSKKAGTPAK
Cardiac	AKVTGRWK
Slow skeletal	GRVGGRWK
fast skeletal	GKVGGRWK

Consensus length = 308

1. Cardiac.....287 amino acids.....(P45379 - swiss prot identification number)  
MESNARD L., *et. al.*  
*FEBS LETT.* 328:139-144, 1993.
2. slow.....277 amino acids.....(P13805 - swiss prot identification number)  
GAHLMANN R., *et. al.*  
*J. BIOL. CHEM.* 262:16122-16126, 1987.
3. fast.....257 amino acids.....(P45378 - swiss prot identification number)  
WU Q.-L., *et. al.*  
*DNA CELL BIOL.* 13:217-233, 1994.

Sequences (1:2) Aligned. Score: 58  
 Sequences (1:3) Aligned. Score: 61  
 Sequences (2:3) Aligned. Score: 63

FIGURE 17C

## Rat Troponin T

Human Cardiac	SDIEFVVREY	EEEEQE...	.....AA	VEEQSEAAEE	DAEAEAEETSE
Rat Cardiac	SDAEFVVREY	EEQEEDWDV	EEDEDEQEBA	VEEDDGEAEF	DPEGEAEAE
Rat Fast sk	..SDEETEQU	EEQYEE...	.....E	.....AQ.	.....EEE
Human Cardiac	TRAEDDEEER	EAKEADGPM	EEKPKP..RS	FMPNLVPPKI	PDGERVDFDD
Rat Cardiac	DKAEEVGPDE	EARDADGPM	EDSKPKPSRL	FMPNLVPPKI	PDGERVDFDD
Rat Fast sk	..VQEEAPEPE	EVQEE...	...KPRP...	...KLTAPKI	PEGEKVDFFD
Human Cardiac	IHRKRMEKDL	NELQALIEAH	FENRKKEEEE	LVSLKDRIER	RAERAEOQR
Rat Cardiac	IHRKRMEKDL	NELQALIEAH	FENRKKEEEE	LISLKDRIEK	RAERAEOQR
Rat Fast sk	IQKKRQNKDL	MELQALIDSH	FEARKKEEEE	LIALKERIEK	RAERAEOQR
Human Cardiac	IRNERKERQ	NRLAEERARR	EEENRRKAE	DEARKKKALS	NMMHFGGYIQ
Rat Cardiac	IRNERKERQ	NRLAEERARR	EEENRRKAE	DEARKKKALS	NMMHFGGYIQ
Rat Fast sk	IRAEKERERQ	NRLAEERARR	EEEDAKRRAB	DDLKKKKALS	SMG..ANYSS
Human Cardiac	KQAQTERKSG	KQTEREKKK	KILAERRKVL	AIDHLNEDQL	REKAKELWQS
Rat Cardiac	K..AQTERKSG	KQTEREKKK	KILAERRKVL	AIDHLNEDQL	REKAKELWQS
Rat Fast sk	YLAKADQKRG	KKQTAREMKK	KILAERRKPL	NIDHLSDDKL	RDKAKELWDT
Human Cardiac	IYNLEAEKFD	LQEKFKQOKY	EINVLNRIN	DNQKVSCTRQ	...KAKVTGR
Rat Cardiac	IHNLEAEKFD	LQEKFKQOKY	EINVLNRIN	DNQKVSCTRQ	...KAKVTGR
Rat Fast sk	LYQLETDFKE	FGEKLRQKY	DITTLRSRID	QAOKHSHKAG	ATAKGVGGR
Human Cardiac	WK				
Rat Cardiac	WK				
Rat Fast sk	WK				

- Human cardiac TnT....287 amino acids ( P45379 - swiss prot identification number)  
MESNARD L., *et. al.*  
*FEBS LETT.* 328:139-144, 1993.
- Rat Cardiac TnT.....298 amino acids ( P50753 - swiss prot identification number)  
JIN J.-P., *et. al.*  
*J. BIOL. CHEM.* 264:14471-14477, 1989.
- Rat fast TnT.....258 amino acids ( P09739 - swiss prot identification number)  
BREITBART R.E., *et. al.*  
*J. MOL. BIOL.* 188:313-324, 1986.

Sequences (1:2) Aligned. Score: 88  
Sequences (1:3) Aligned. Score: 60  
Sequences (2:3) Aligned. Score: 59

Consensus length = 302

## FIGURE 17D